Program and Abstracts

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1

Characterization of the Transmission of Alfalfa leaf curl virus, an Aphid-transmitted Geminivirus

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Abstract

For decades, whiteflies, leafhoppers and treehoppers were the only known vectors of geminiviruses (family Geminiviridae). Metagenomic analysis revealed four divergent members of this family that are now classified in a new genus named Capulavirus according to their type member Euphorbia Caput medusae latent virus (EcmLV). Among them, Alfalfa leaf curl virus (ALCV) infects mostly Fabaceae and has been shown in our lab to be transmitted by *Aphis craccivora*. As it was the first report of an aphid-transmitted geminivirus, the mode of transmission was characterized. The transmission journey of ALCV starts in the phloem (Vicia faba) where it was shown to be restricted using FISH and EPG. To reach a 50% transmission success it needs at least 10 insects per inoculated plant following an acquisition access period of at least 24 hours. Once the aphid has acquired virus, the viral load remains constant in its body and transmission was still possible up to 11 days post-acquisition. Viral DNA was detected in the midgut and salivary glands which altogether support a circulative persistent mode of transmission involving internalization into insect epithelia mediated by potential receptors. The relatively low transmission efficiency of ALCV may be explained by the non-uniform distribution of ALCV (FISH and EPG) which may hinder its acquisition, and a non-efficient release from the viruliferous aphid into the inoculated tissue as revealed by qPCR. The aphid transmission of ALCV is highly specific because *Aphis tirucallis*, a close relative of *A. craccivora*, undistinguishable with CO1 phylogeny (Coeur d'Acier *et. al.,* 2014), did no transmit ALCV although we identified it as the vector of EcmLV. Thus, we compared the pathways of ALCV between the two aphids to enlight potential transmission barriers in *A. tirucallis* body (qPCR, FISH), and initiate the identification of potential receptors in *A. craccivora* with a Y2H approach.